Abstract: Described herein is a method for the detection of cyto-sine methylation in DNA samples, wherein the following steps are conducted: a genomic DNA sample, which comprises the DNA to be investigated as well as background DNA is treated with bisulfite (= disulfite, hydrogen sulfite) in such a way that all of the unmethylated cytosine bases are converted to uracil, while the 5-methylcytosine bases remain un-changed; the bisulfite treated DNA sample is amplified with the use of at least 2 primer oligonucleotides as well as a polymerase, wherein the DNA to be investigated is pre-ferred over the background DNA as the template, and a control fragment is amplified simultaneously to the am-plification of the bisulfite treated DNA within the same reaction mixture the amplified products are analyzed and the methylation status in the DNA to be investigated is concluded from the presence and /or the amount of the amplified products and/or from the analysis of additional positions.